

# From QSAR to Big Data: Developing Mechanism-Driven Predictive Models for Animal Toxicity

**Hao Zhu**

Department of Chemistry  
The Rutgers Center for Computational and Integrative Biology  
Rutgers University-Camden  
Email: hao.zhu99@rutgers.edu

September 24, 2015

# Acknowledgements

## Rutgers:

- PhD students: **Marlene Kim, Wenyi Wang**, Daniel Russo, Linlin Zhao
- Master students: Kathryn Ribay, Joe Hess
- Visiting Scholar: **Dr. Aleck Sedykh, Dr. Jun Zhang**

## John Hopkins University:

- Dr. Thomas Hartung

## Shandong University:

- Dr. Bing Yan

## NCATS:

- **Dr. Menghang Xia, Dr. Ruili Huang**

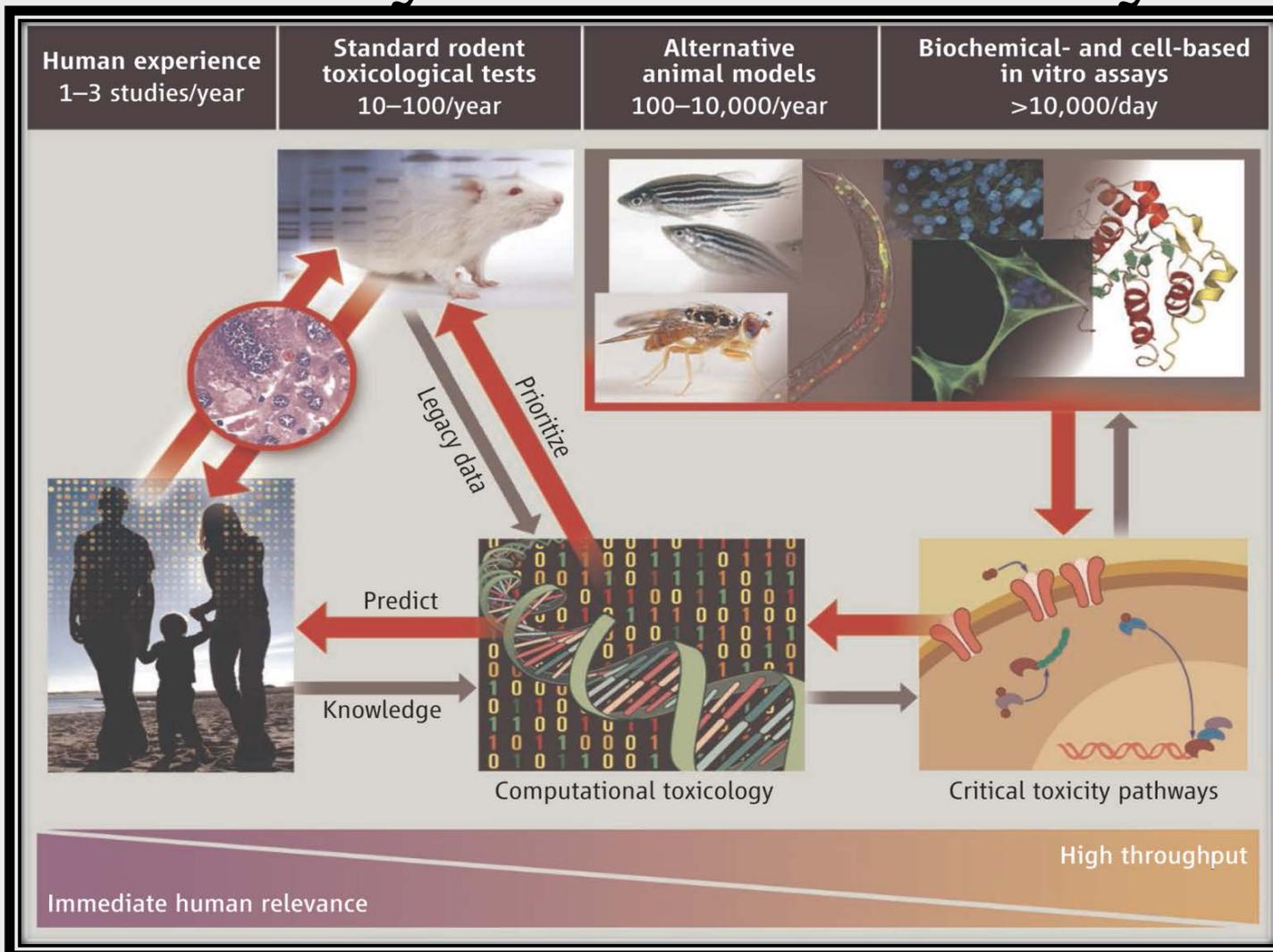
## ICCVAM:

- Dr. Judy Strickland

## Funding resource:

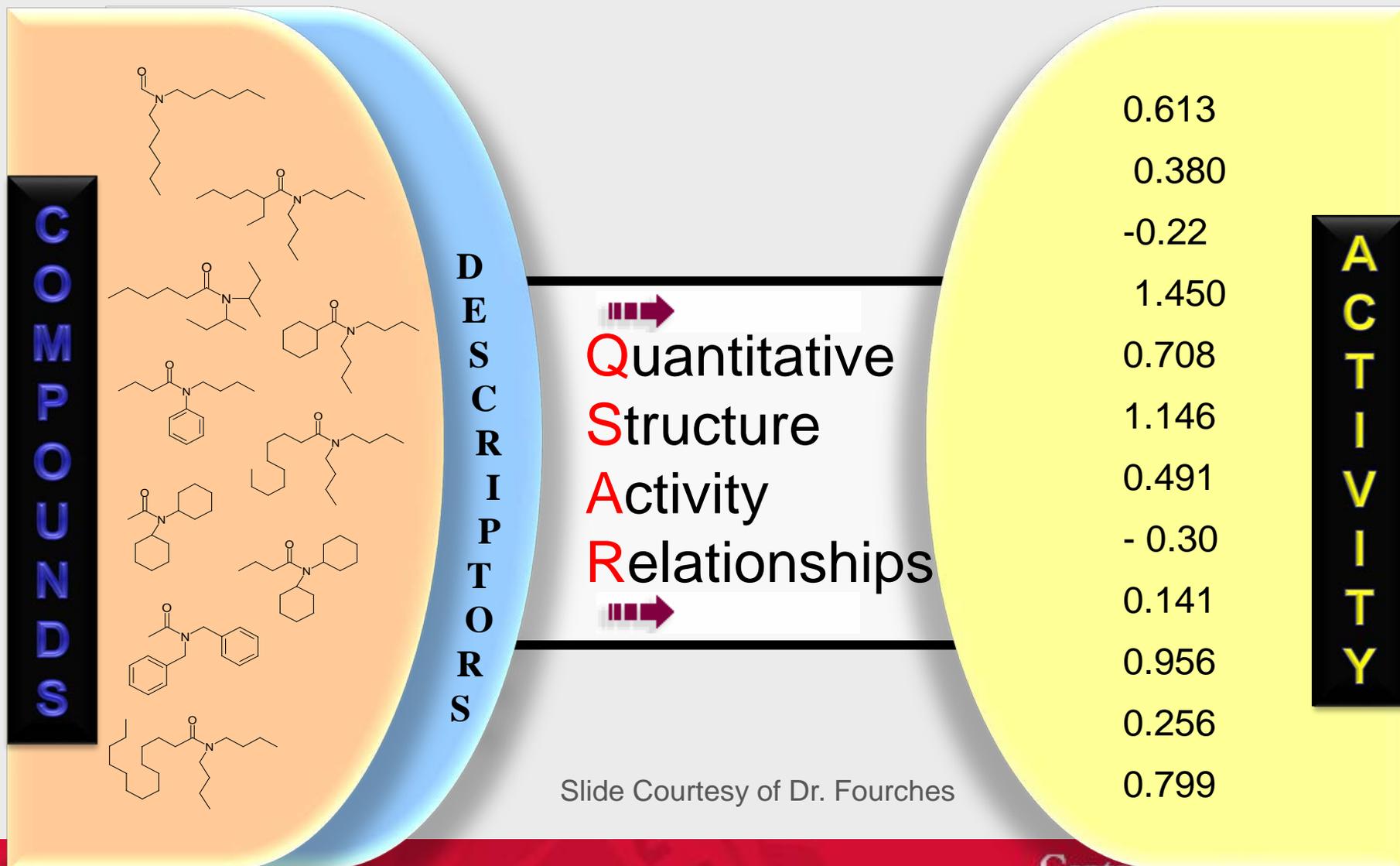
- National Institute of Health: 1R15ES023148
- Society of Toxicology: Colgate-Palmolive Grant for Alternative Research

# Toxicity evaluation today



Collins, F. S., Gray, G. M. and Bucher J. R. *Science*, 2008, 319, 906-907

# Principles of QSAR modeling

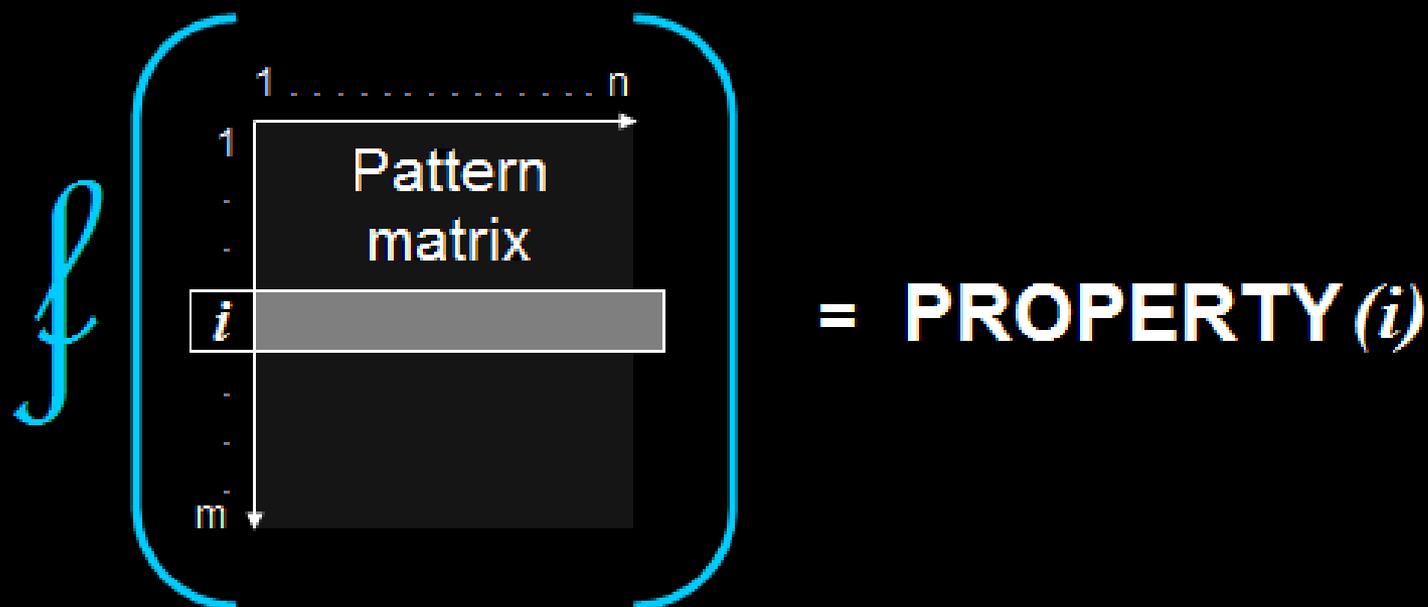


Slide Courtesy of Dr. Fourches

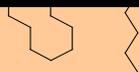
# Principles of QSAR modeling



0.612

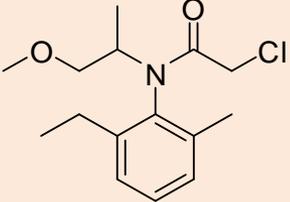
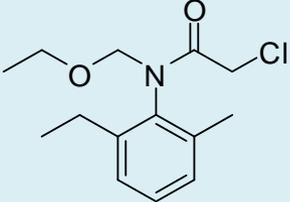
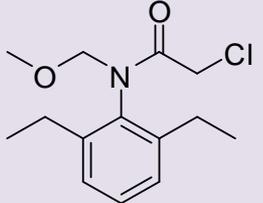
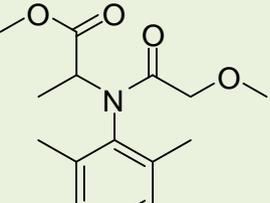


With  $m$  molecules and  $n$  descriptors

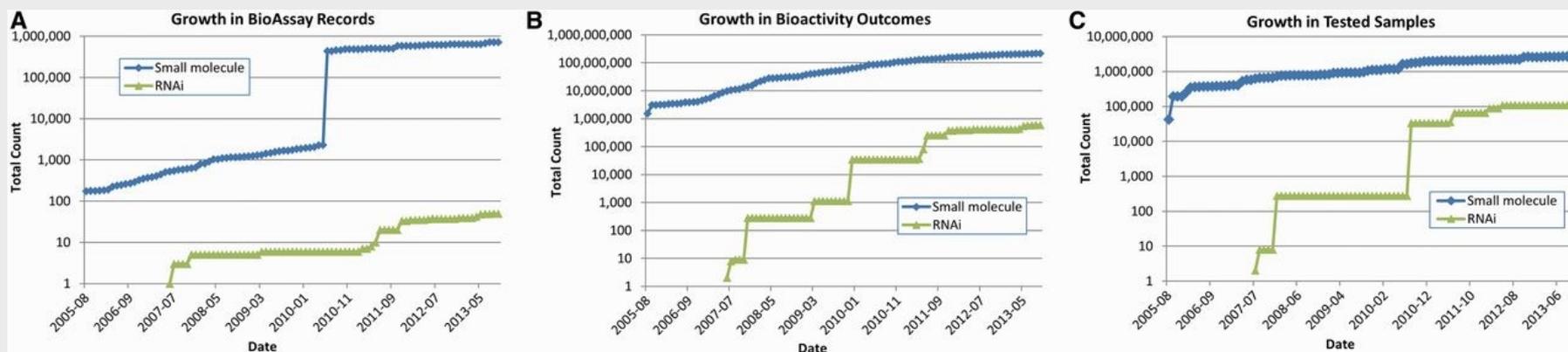


0.799

# The “similar” compounds that have “dissimilar” toxicity profiles

		IN VIVO ASSAYS				
		MOUSE_KIDNEY	RAT_SKELETAL_AXIAL	MGR_RAT_LIVER	MGR_RAT_KIDNEY	
<p><b>NOTES:</b>            0: non-toxic/inactive            1: toxic/active            -: not tested            NN: Nearest Neighbor</p>						
METOLACHLOR		0	0	0	0	
		1	1	1	1	
NN2-ALACHLOR		-	0	-	-	
		0	1	1	0	

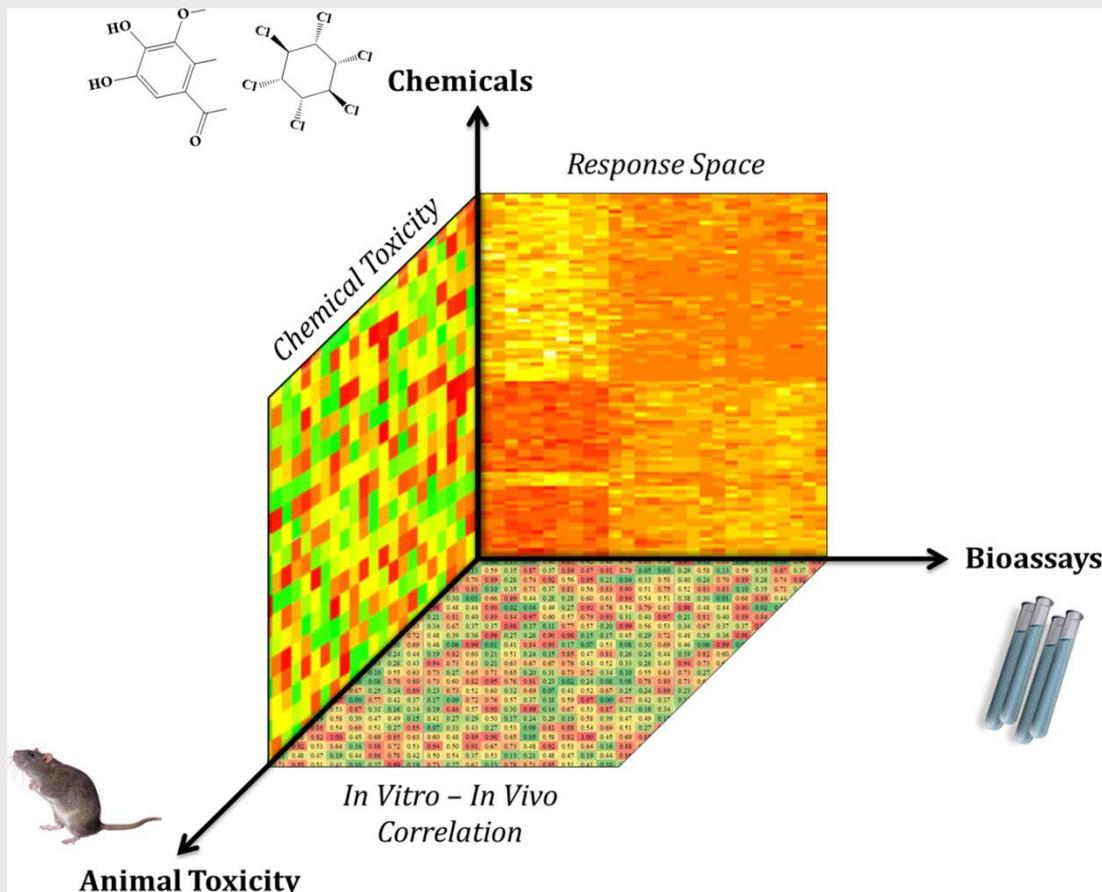
# PubChem data in 2014



- >700,000 bioassays
- >200,000,000 bioactivity outcomes
- >1,200,000,000 data points
- >2,800,000 small molecule samples
- >1,900,000 chemical structures
- >108,000 RNAi reagents

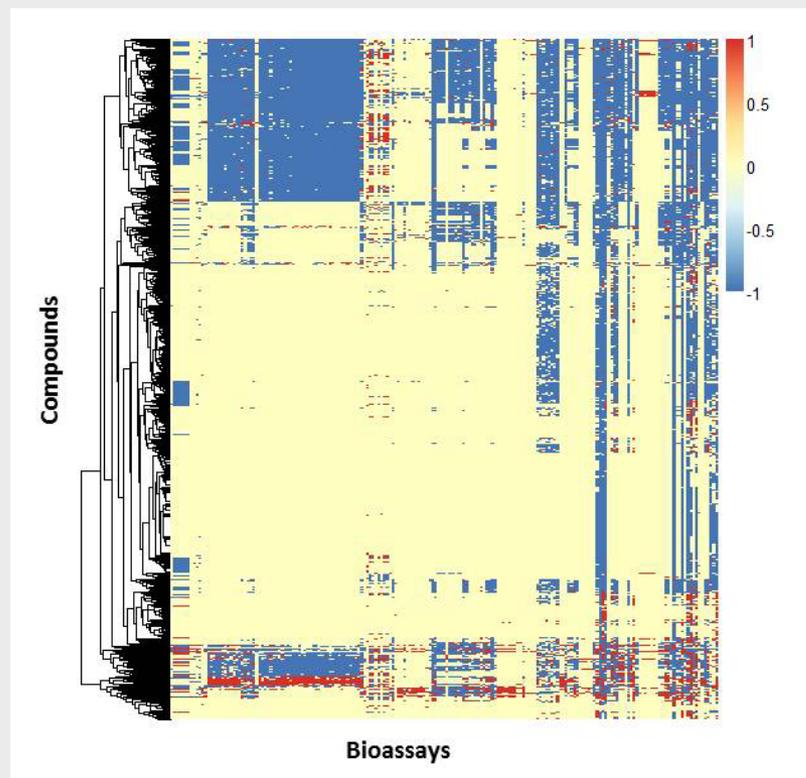
Yang et al. *Nucleic Acids Res.* 2014 Jan;42: D1075-82

# Chemical-in vitro-in vivo profiles in big data era



*Chem. Res. Tox.* 2014; (27) 1643-1651

# Before the ToxCast project, data already existed



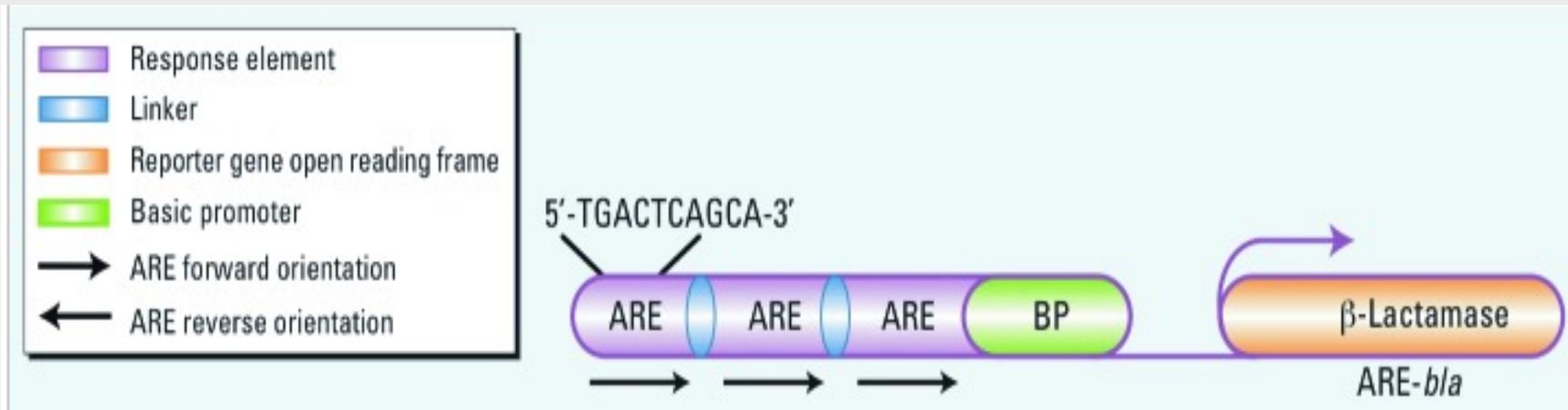
Obtained from PubChem on Aug. 1, 2013, before the ToxCast phase II data was released.

# The current question is:

- What can we do if we have limited in-house data available for the compounds of interest?

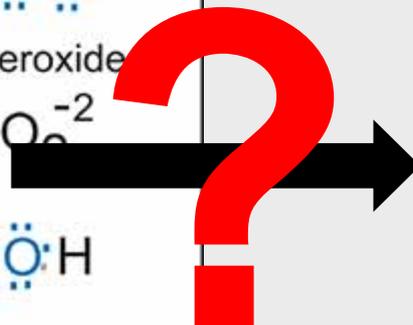
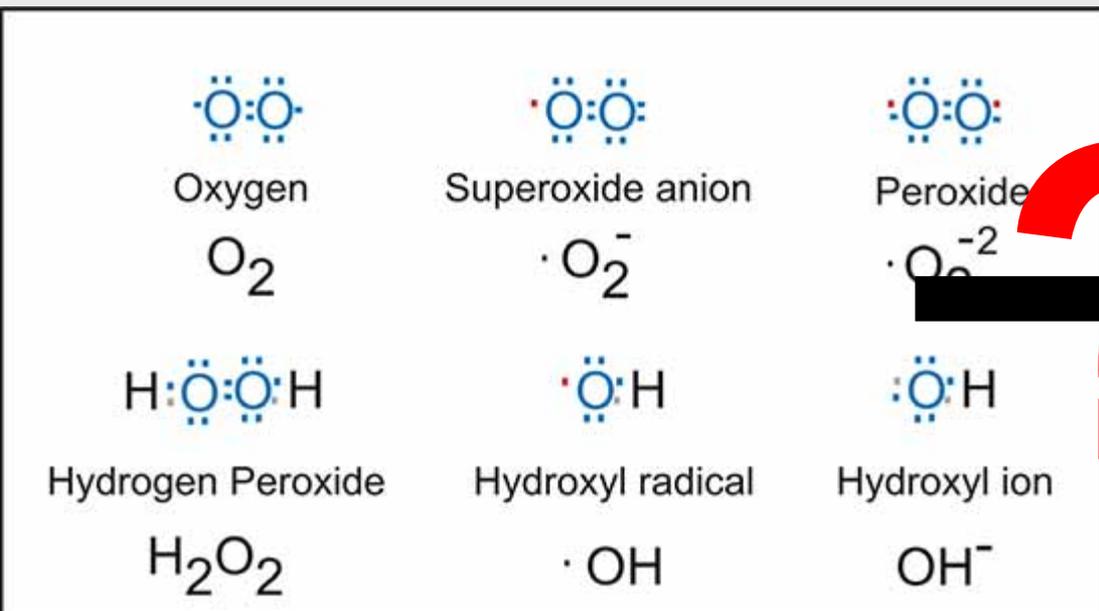
# Antioxidant Response Element $\beta$ -lactamase reporter gene assay (ARE-*bla*)

- Recognized by the Tox21 program as one of the most important toxicity assays
- ARE genes play a role in alleviating oxidative stress



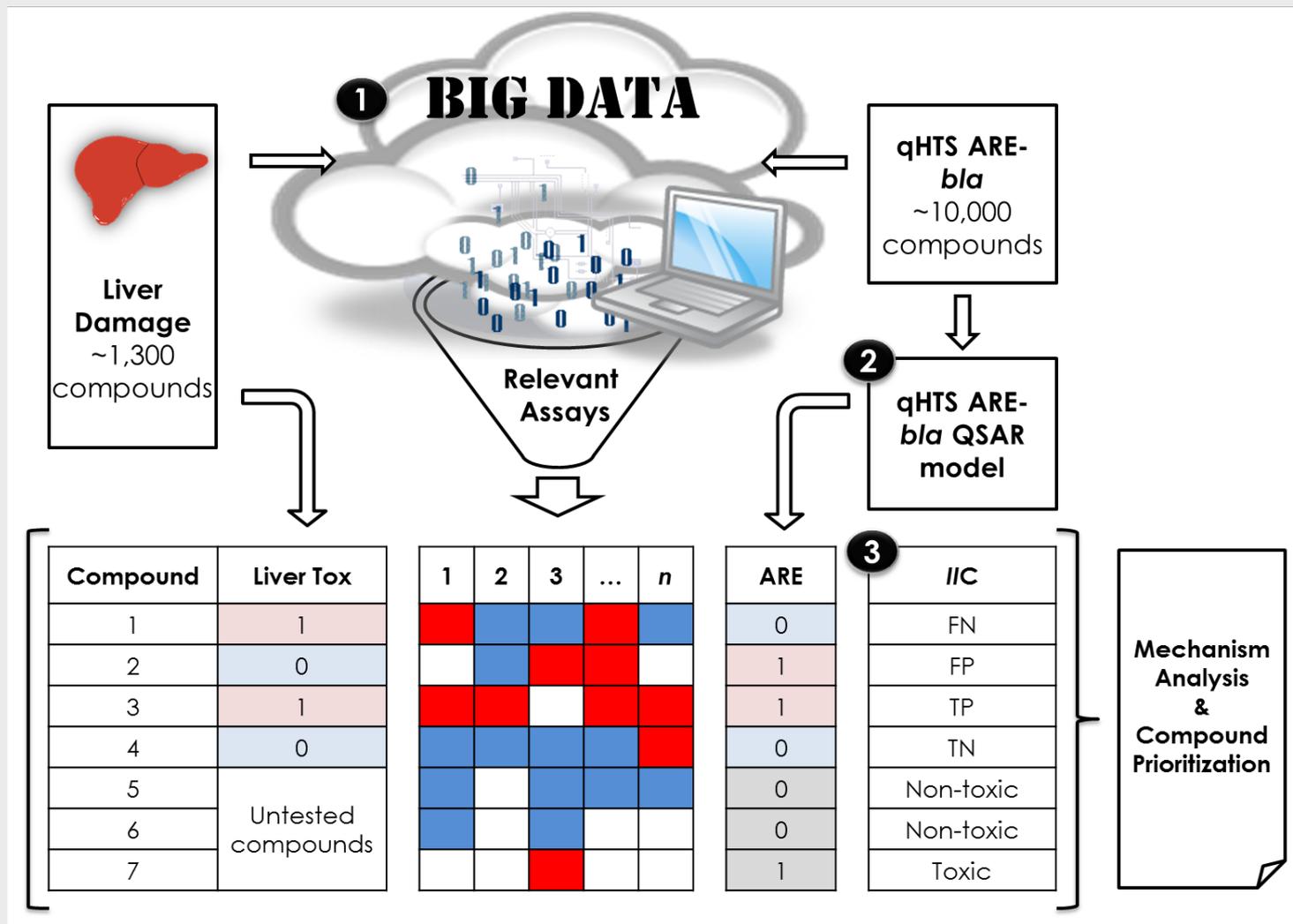
Shukla SJ, *et al.* Environ Health Perspect. 2012, 120(8):1150-6.

# Reactive Oxygen Species (ROS)



**Liver damage**

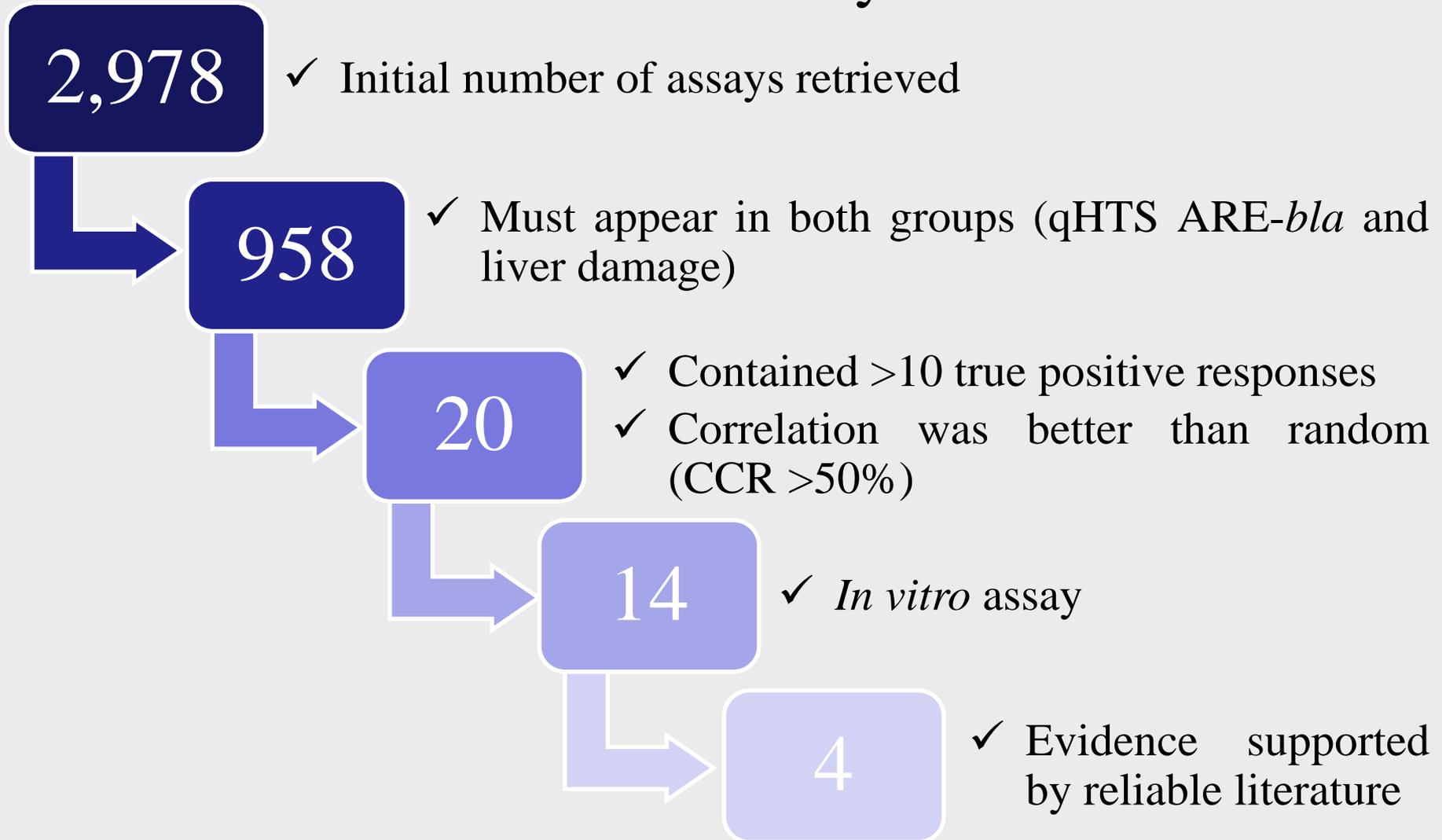
# Workflow for profiling liver toxicants



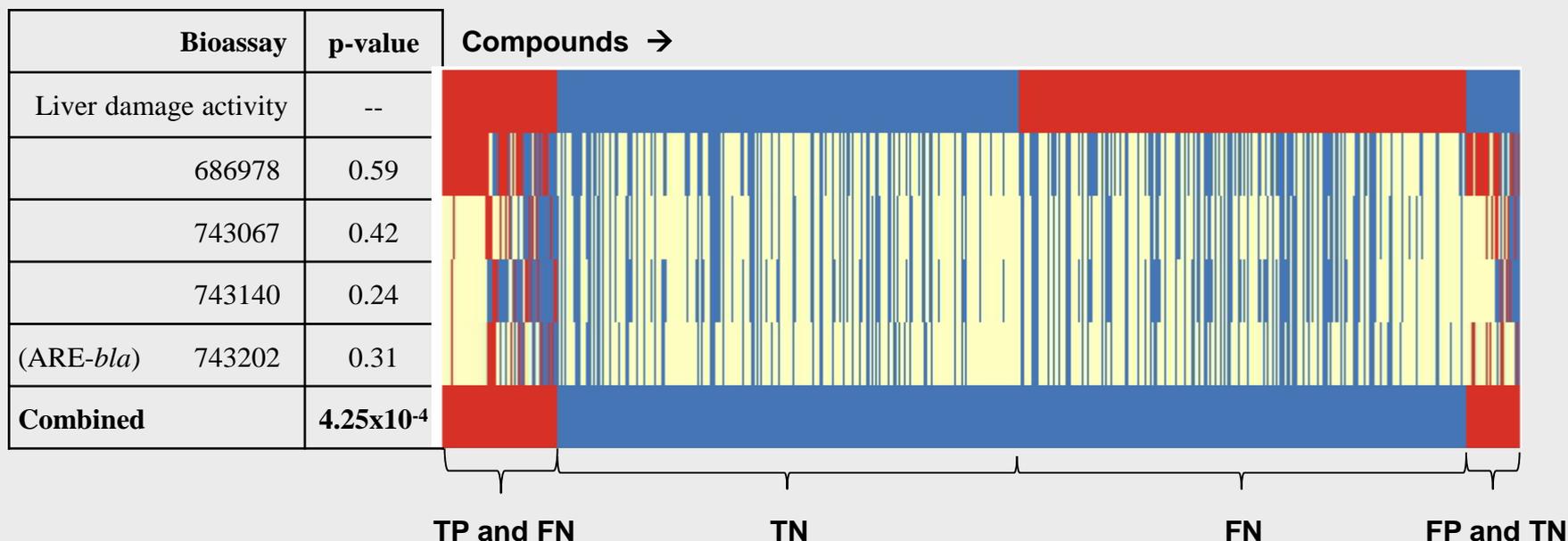
## Profiling target compounds with biological responses using automated tool

- Input – target compounds:
  1. qHTS ARE-*bla* dataset (10,928 compounds)
  2. FDA liver damage dataset (1,314 compounds)
- Output – assays related to:
  1. qHTS ARE-*bla* activation (1,819 assays)
  2. Liver damage (1,159 assays)

# Criteria for filtering inadequate and finding relevant assays



Individual assays showed poor IIC, but the combined response using  $RA > 0.25$  show statistical significance



- Active or toxic
- Inconclusive or untested
- Inactive or non-toxic

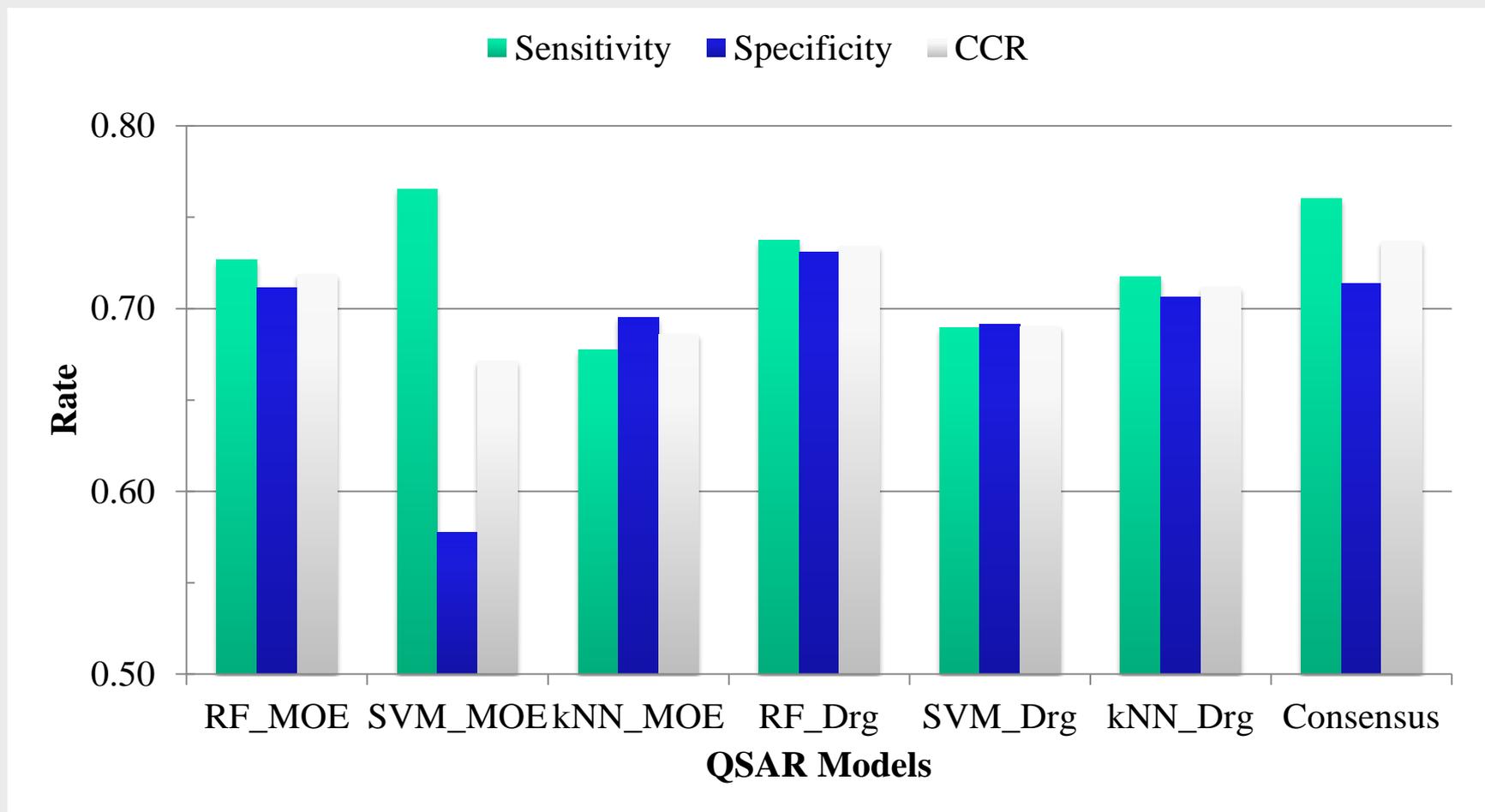
Rate of actives (RA)

$$RA = \frac{A}{A + I}$$

A = no. of active responses

I = no. in active responses

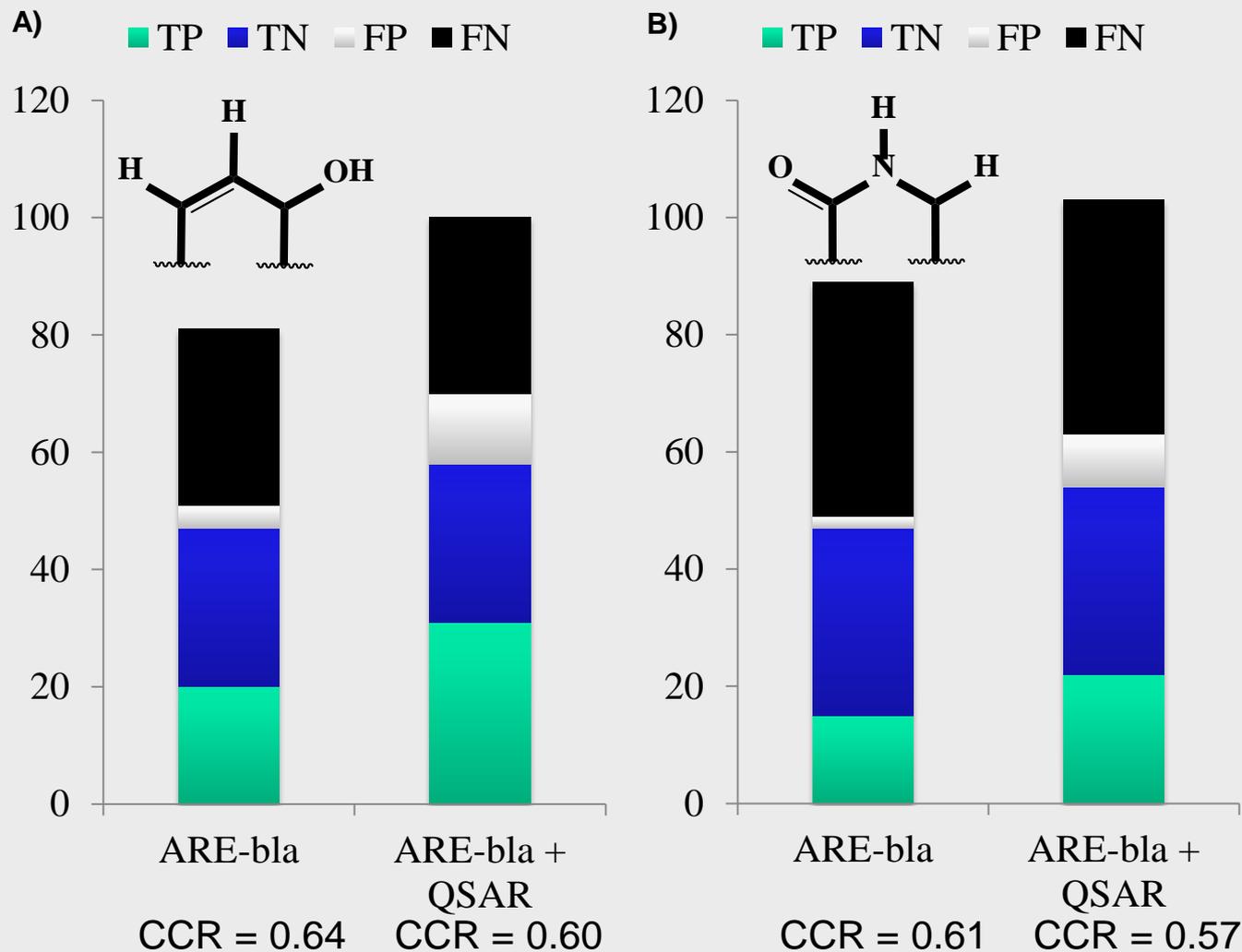
# Modeling qHTS *ARE-bla* activation using QSAR approaches: 5-fold cross validation for all individual models



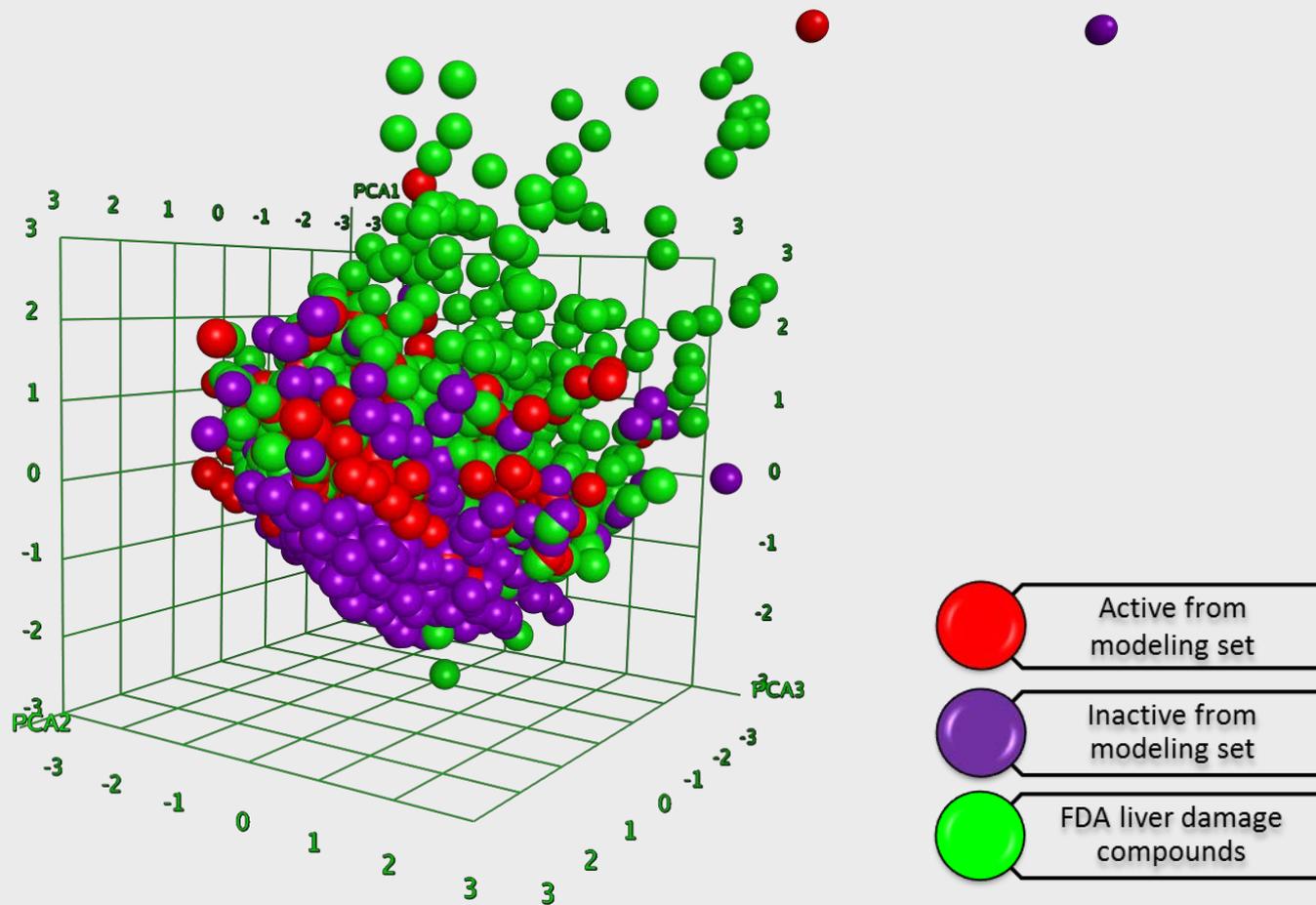
# Evaluating In vitro-In vivo Correlations (IICs)

- Focused on compounds that were active in qHTS ARE-*bla* and liver toxic
- Searched for common chemical features
- Evaluated IICs (sensitivity, specificity, CCR, and  $\chi^2$ )

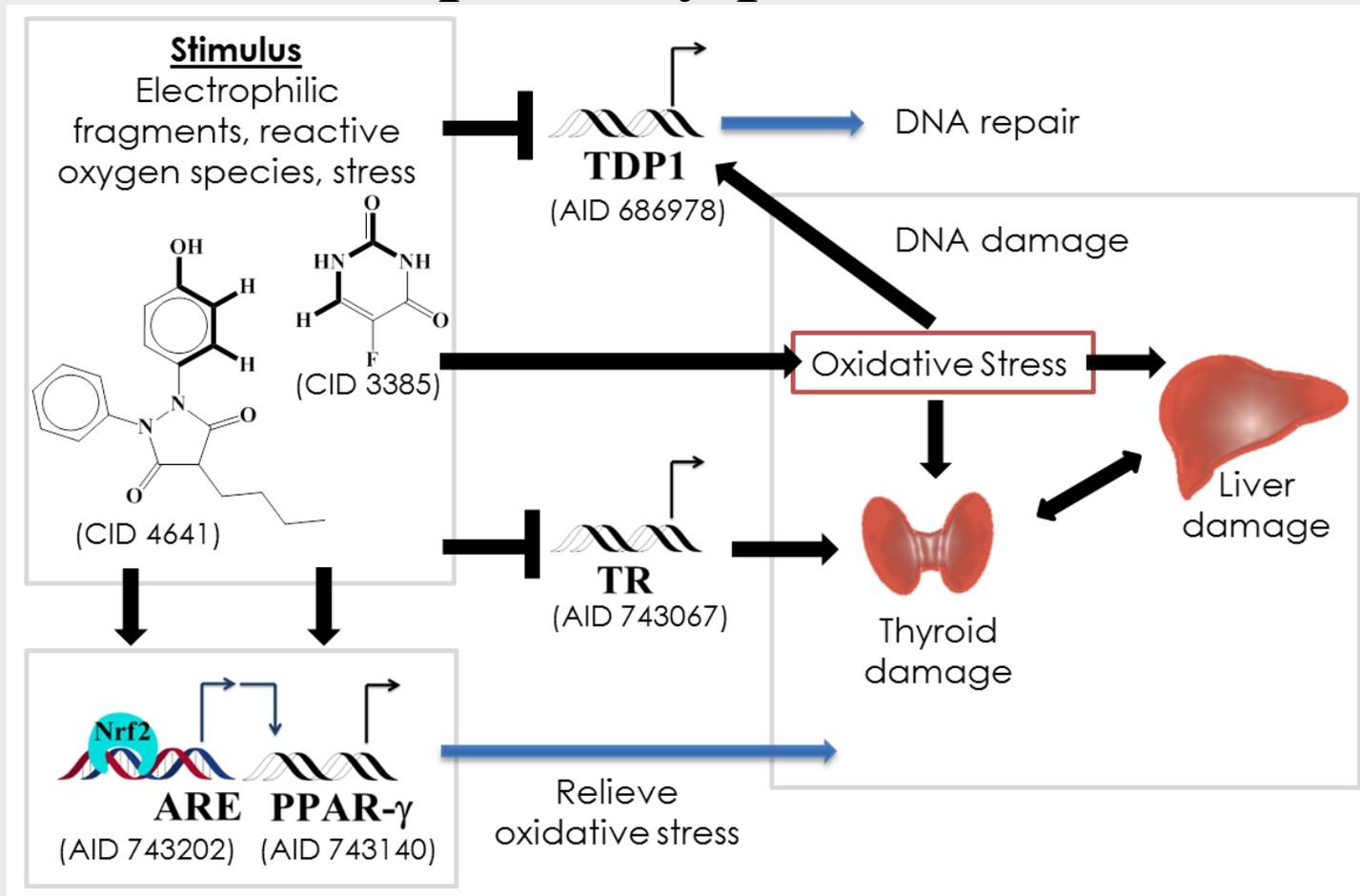
# IIC between qHTS *ARE-bla* activation and liver damage for overlapping compounds containing the toxicophores



# 3-D plot of Tox21 phase II modeling set vs FDA liver damage dataset using principal components analysis



# Liver toxicity mechanism analysis involving ARE pathway perturbations



# Conclusions

- Developed a workflow
  - Profiles biological responses from big data
  - Incorporates QSAR models to fill-in missing data
  - Evaluates the chemical IIC
- Identified toxicophores and assays that can be used to assess liver damage induced by oxidative stress
- Workflow can be adapted to model or assess other complex animal toxicity endpoints

Mechanism profiling liver toxicants by using antioxidant response element assay data model and public big data. *Environ. Health Perspect.* In press

# Take home message

- Reliable information exists, but it is difficult to locate
- Good data may not guarantee good decisions